

Detailed description: This figure is a sequence logo plot showing the conservation of amino acids across 190 positions. The x-axis represents positions 1 to 190. The y-axis lists 20 proteins. Each protein's sequence is shown as a vertical bar where each segment's color corresponds to a different amino acid. Conserved amino acids are highlighted in green, while variable ones are in blue.

410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600

30694992.p KE EVALP APIAKLNTVQEENDDTSFSSPDKSSTDDVESGLFQ-NEKKES NLQDDTAEDDSNSESESLSGSWSSDLSAQDQVQISKKDLLMVHLLRVCSTS RGPFLADALPQTDELH ELGLSSEBVIDLASKS

39930006.q GQ KNIMKHDVIRETSLVEEETENSDTIVNTSNTGTPERFSSVHQLEDS DLSGGWDNDEDSGGSGSSPFDFMFDDASRNKKDLILVHLRLACASDKSLSAFLPKEISLCC-NIGLSEWAKDLSLQSKP

6981046.m DC MKVLREVKVLAGLQHPNIVSYHTAWIEHVEVLPQ-QDRVPILPSELEVSLQEEGD-RNQQGVKDNESSSS-IIFAELPTPEKENPALESDVKUNNNNSYVRANLVRISSESSESSIELQEDGLN-ESPLRVPKVHQLPLGHS

7305015.m DC MKVLREVKVLAGLQHPNIVSYHTAWIEHVEVLPQ-QDRVPILPSELEVSLQEEGD RDQGGVKDNESSSS-IVFAELPTPEKEKPFGESEVKENNLLVSYTANLVRVSSESESSIELQEDGLT-DLSVRPVVRHQLPLGHS

HRI.h VC MKVLREVKVLAGLQHPNIVSYHTAWIEHVEVLPQ-QDRVPILPSELEVSLQEEGD REQCVKVNQKDFDNESSSSIIFAEPTPEKEKPFGESEVKENNLLVSYTANLVRVSSESESSIELQEDGLN-CTKIKLTLSKAAKSXAKVWYKPSALMDSL-SLAPLLEVLQKFQKSDP

32412400.y ISD'TDSSAPTIWTSILTPLATKQPTEELLDDLAG-HIDTNKAKTDALLELAFLFENNGIHQDHLH PANLYRNEAGDVKITPDSTFYCERELHN- CSSRAVTALRDAKSAXWLPEPIAGTAKPHYTQKDIDFGVMFLQMVFDLAFQDLCFKKCCVCLDDKWRSPQKLKHSP-LSSEMELBLVSSFFHSE

39947974.y VCSVDGVSPD-RTVSILTAYAKQGSYLDHMVNGDQGQIGINRVRSTRDLLDALNFIHTNGIVHKSIHPHNVLLFRDTEGAIIPLSVEVSDQEE- CSSTGKDNESSS-IIFAELPTPEKENPALESDVKUNNNNSYVRANLVRISSESSESSIELQEDGLN-ESPLRVPKVHQLPLGHS

34856678.r VRYFAMNSREEDSIVVDILAEVSGCISLATHSHSGPVPMHOLRKYTAQQLLAGIHLRNSVWVHKVLSTASVLDLDAEGTIVKITYDTSISKRLADICKEDVFETQRVRFSDSALPYKTKGGDVRVLLLSSLQSQCEYVTTIPSLPDAFQDFLKCCVCLDDKWRSPQKLKHSP- NPQKXMPFLVQESEPDIG

7305017.m VRYFAMNSREEDSIVVDILAEVSGCISLATHSHSGPVPMHOLRKYTAQQLLAGIHLRNSVWVHKVLSTASVLDLDAEGTIVKITYDTSISKRLADICKEDVFETQRVRFSDSALPYKTKGGDVRVLLLSSLQSQCEYVTTIPSLPDAFQDFLKCCVCLDDKWRSPQKLKHSP- NPQKXMPFLVQESEPDIG

GCN2.h VRYLAMNLKEODDSIVVDILAEVSGCISLATHSHSGPVPMHOLRKYTAQQLLAGIHLRNSVWVHKVLSTASVLDLDAEGTIVKITYDTSISKRLADICKEDVFETQRVRFSDSALPYKTKGGDVRVLLLSSLQSQCEYVTTIPSLPDAFQDFLKCCVCLDDKWRSPQKLKHSP- NPQKXMPFLVQESEPDIG

17137328.f VSYECVLCQIKRKLEGGLVYLVSISSSLG-WCMQGARVGLDALVFLHNGVWHSKLLDTWMDNTCNVRVSDFSLNVNLLLELLSG AGQSSSCGDLPALGALVESLMPIN SYEMRDFVDCNCSD-RTLSASELSPHPL-RFYUDNCQVLLQHTPSSVQILFQEDSVADLTCYPCNSTCNLTDLFKKAEDQDYAESDCSSTTS

6320489.y GRNNATFWKR-LLTECYNNPPGLDIQSQVGFVNLTARDWMLRLECLEAHKLGLVWHSKLLDTWMDNTCNVRVSDFSLNVNLLLELLSG MLERYNKGNSVLLPESTWIAPLKFNNAKPQLRTDIOWLQVLFIQTSISGDIVMNFTPEOFDLSTS-MDTELTYDLE-KMLNNPDR

19112783.y TRGYG -WRLYLVQLEYSPKPTLEFLSLQTLVLTLDVETVRAFSNNILDEGLAELHRLGIHSKSLHLDNWLFLHSGHETRFAKLMDFGFTIRTLRDMN- ASHFNFNINSQSIINILPCEGLYPPESSEFAASRKTIDWCFGLLVLQMLQGAAVILNFKFSSLKIMTHVPLLLPGSVDLVRCLMRDSCSSTTS

113r_PKA -GNAAAAKKGE -QESVKEFLAKAK

19114058.y YS KIFREIKCLAKMDHPNVIRYFSSWESTTEATQMPIVMSK -NSSRVLGTSYYCDVNGMDSIIFEPTESSALTTDDILFAEDPGTESIISTSRKSSYSSSTESS-NFENLESPPRNLLDGSV- TS SNIFRESRTLARINHPNVIREFSSWVLEQSSKEQTEERPLASADETLSQSADDIN FMFDMDTGLLQHHTYPPSSVQILFQEDSVADLTCYPCNSTCNLTDLFKKAEDQDYAESDCSSTTS

2erk_Erk2 -AHHHHHHMAAAAAGPEMVRGQVFDVGPR-YTNSYIGEGRAY

1jwh_CKII -MSGFVPSARVYIDVNTHR-REYWDYESIVEWBGWY-DDYOLVRLKGRKY

17537697.w HLTGWSVTRNRSQDCVFRPSDFGSMQPLLDLVKMPGDFICSGKYYVARDEDEKEKEYDRRRKDLFOLGTLIDGL-LATRGSTSRSVPPTPVEGNONTGTLNLLG-NFIAKQCQAEAKNIDQLOVEDPFLKEECQGSESENIFTPFGGAMS PDRMLADNVIIRLGRGGFDVVVLNRKMDSTDYAKRIPNAKSDKLN

67210013.q -MPLKWLSPNPPNSSDCYFCLWPSCGQSKATKSYSLQWLRYDNKBEALGFGFINKE-QQRNRIKDAEILLSTMFTNHWKTLGMLCKLBEFGHLPLNLCDSMGMGPNPSMDNFKINKLNGKGR-YEVVVECTYNSG

83524413.q -GAVGDDAERGGETWEKAAEIEGEGAMSRDENMETLESEEKEEEEISGSSDETE-EEGEHGHKKYSSVQIRMWPQGIPRVRVWLKQEVGKVLKTTIAIAPEIDDDKTTQEFSDDLKHLKCAKISAND

23509645.z NQK DNIIESVIIVKDKKDRANNHISEQMDKYEKVNVEELSKHINNNKNNVVEDVSVLSY LDEEISIEQDKDHHFFSDRKRQDEISINFQMEENIDMNNDMNDINMKGKXXHKGKQVDEKYOIDDDKKKKRPFYRNWNNDH-LTQLQAN

lias_TGFbR -EDPSLDRPFISEGTTKLKDLIYDMTTSGSGSLPPLLQVORTIARTIVLQESIG-KGRFGEVNRGWK

83602017.q -ANDLVECVELELTNGEHERTSNILEIIEPLKATAVLTSYDTAQG-MSVLWRSTTIVSVSMLDKVKSVVLSNSDALKMFATVIRFRGHISKDSFYPLAIDFK-RDFVPTGILGK

43460021.q -ASVCVQEMVITMVSADDVYSSLMPVHALSDPGTALPDANSYFSISIHPVEGR-CVLIKHYQNRGESEKQWVSTSIYYLALINSLEDDLGEDPIELDSDPEDALKGDFIELHGQISMEIHMPLMFLKQFQK-DYRCEKQIGKGSE

610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800

30694992.p PDFNRTFEEHANQNMASTSVQFWEPSS DSCEPNAISLPSRYYLNFEELKICLQGFGHVVLCKNKLDGRQYAVKVKRDKDE IPUNSRIV

39930006.q AVFGETFCHFFGPQMTCSECSLFWR -ADNSSSRPNSYRVLNPDEEIRSLCQGFGFGRVALCKNKLDGRQYAVKVKRDKRS- PONNEKILSLLQCEANVQTINIVHVAVD

6981046.m SDVEGNFTSTD- ESSEDDNILIGC LSEWDWIAE

7305015.m SELEGNFTSTD- ESSEDDNILIGC LSEWDWIAE

HRI.h SHLEESFTSTD- Q3DVRVYHMLHOMOLCE LSEWDWITE

32412400.y KKR-RAFELSSSEPLATN-APIIIDDDED-IAPVFGSLMPMPQ- MTPQQRMRDHSMSRGPMS-SRYRDTWVPEAKRQGFCGEVVRARKRMDGHLVYKXKGTORSQET-LS -EILKEVRLRSLQMNHSFAPURYINTWLEEVPDYADTEGDTSTEGG-

39947974.y SRRRAFPLGSHHFLAATSAQVLMDDADSSVTFADSVSSMPQ- HVPVPLRHSMSRATAPSRVANEWIEBGRKICQGFGCEVVKARNMVENVYVYVKRDKRGENES- LT -PIIIEVSFVCRMGRHES-PVKVYMAWIEDIFDGYEPSSAGSVITASG

34856678.r GQDYIETIPIVNSQNLPSAA- FFSETQKPSRFYFIEPEELQKLGCAFCAVVKVQNKLDGCCYVVKRDPINPASR-QFR- RIKGEVTLTSLRLLHENEIVRYYNAWIERHERPAGVTPPPDCTQADOPATCKTSQGD

7305017.m GQDYIETVIPSQNLPSAA- FFSETQKPSRFYFIEPEELQKLGCAFCAVVKVQNKLDGCCYVVKRDPINPASR-QFR- RIKGEVTLTSLRLLHENEIVRYYNAWIERHERPAGVTPPPDCTQADOPATCKTSQGD

GCN2.h GQDYIETVIPSQNLPSAA- FFSETQKPSRFYFIEPEELQKLGCAFCAVVKVQNKLDGCCYVVKRDPINPASR-QFR- RIKGEVTLTSLRLLHENEIVRYYNAWIERHERPAGVTPPPDCTQADOPATCKTSQGD

17137328.f QHNPVQRTGSMAMPYQT- TLALS-SRIRTPEEVYIILKLGCAFCAVVKVQNKLDGCCYVVKRDPINPASR-QFR- KMTNTERVELLSRLHENEIVRYYNAWIERHERPAGVTPPPDCTQADOPATCKTSQGD

6320489.y KRKLGTIELLMPKFLRINIDSTINRFLVLESVYNENSLELTPGDTITVRGNQGRILSQQSITRRSFNVGSRFSSINPATRSASPEETAVIICQGAFCAVVKVQNKLDGCCYVVKRDPINPASR-QFR- TILSEVMLLAQHNYQVYVYAAWETEDMDENVFESTDEESD-

19112783.y RKRPSAIDLSSHIVRLGTVAPPVEQGTFSKSARPSYGGQQ- DGIIIDLLYRKVSRYEITFECIPEFRRGGFCEVVKVKNRMDGRFLVYKVKLVSLLDSDK-ENS -RILREVMTLSRLHENEIVRYYNAWIERHERPAGVTPPPDCTQADOPATCKTSQGD

2phk_PKA CK TAQLDQDFRHKICLQGFGFGRVALCKNKLDGRQYAVKVKRDKVKKV -GHPNIIQKRD-T

113r_PKA EDFLKKWETPSQH- DYSSSMHISKQGPHTSFIYIOMQLCPCDDLESYLIRRHNIF- LKQHETLINE

19114058.y STFNNTTILDD- FLSPREDECNTIFSPDQPLCLYIOMALCEETLEKHNRRNPK -H-HGVMSKG

2erk_Erk2 ASEMLLMDS GMVCSAYDNLN- KVRVAIKKQGFEHQTYCQRLTREIKHLRFRHENHGNINDI

1jwh_CKII SEVPEAAININ- AVPIPKEKIGKKGKLTKGKSLDEKRNKANQCGGDSLMPMNRHDSICVDEAKEWSTPFGPKPEG- PKCASRMQSKRSTPSGGLKHLSECSDDDDDSSEIDWDAE-

17537697.w RKIAKEPKAFLNHPNMVRYYYAWAEDLIPIVEETSDDDSSLG- YFDEP-REVSIQMSCLQDANIVTFYQACNEENKEKKNFHGFPG- YFDEP-REVSIQMSCLQDANIVTFYQACNEENKEKKNFHGFPG

67210013.q QYAVKTIDVIN- KEPFRVKIMSCIKAPCVVSYFQAWITD- PKCASRMQSKRSTPSGGLKHLSECSDDDDDSSEIDWDAE-

83524413.q VRVKKLLENNFDMDAINN- SRYYRDPGKFCGGFGYVVMKVKNNKPEFVYQTSKELRSLXQYNTQTNNKHINEKDNNSYIMEAIIAKLQHENIYRYYDAWEEVDFFLYKELQNEFKN- SRELRWSFREAIYQTVMLRHEILGFLIAADKNDGTWTQ

23509645.z KGNELCKKEMN- IMPLAVKIVSKERKGNSCEVEMAKRSGCANHVVYMCWANSEA- EYVSESTWASHCPTDVSTALIYDLYSAWTFEEKKK

lias_TGFbR AHGSVYRCRSR- GFWVVKCTSRPSPHCPATK- EYVSESTWASHCPTDVSTALIYDLYSAWTFEEKKK

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